● o5-90
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RAW SEQUENCE LISTING   DATE: 06/28/2002
PATENT APPLICATION: US/10/081,864   TIME: 10:33:12

Input Set : D:\seqlist.txt
Output Set: N:\CRF3\06282002\J081864.raw

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 4 <110> APPLICANT: Lukyanov, Sergey
 5         Lukyanov, Konstantin
 6         Yanushevich, Yuriy
 7         Savistky, Alexandr
 8         Fradkov, Arcady
10 <120> TITLE OF INVENTION: Non Aggregating Fluorescent Proteins and
11         Methods for Using the Same
14 <130> FILE REFERENCE: CLON-067
16 <140> CURRENT APPLICATION NUMBER: 10/081,864
17 <141> CURRENT FILING DATE: 2002-06-19
19 <150> PRIOR APPLICATION NUMBER: 10/006,922
20 <151> PRIOR FILING DATE: 2001-12-04
22 <150> PRIOR APPLICATION NUMBER: 60/270,983
23 <151> PRIOR FILING DATE: 2001-02-21
25 <160> NUMBER OF SEQ ID NOS: 30
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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30 <211> LENGTH: 687
31 <212> TYPE: DNA
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37 acgcagacct cgacttttaa agtcaccatg gccaacggtg ggccccttgc attctccttt 180
38 gacatactat ctacagtgtt caagtatgga aatcgatgct ttactgcgta tcctaccagt 240
39 atgcccgact atttcaaaca agcatttcct gacggaatgt catatgaaag gacttttacc 300
40 tatgaagatg gaggagttgc tacagccagt tgggaaataa gccttaaagg caactgcttt 360
41 gagcacaaat ccacgtttca tggagtgaac tttcctgctg atggacctgt gatggcgaag 420
42 atgacaactg gttgggaccc atcttttgag aaaatgactg tctgcgatgg aatattgaag 480
43 ggtgatgtca ccgcgttcct catgctgcaa ggaggtggca attacagatg ccaattccac 540
44 acttcttaca agacaaaaaa accggtgacg atgccaccaa accatgcggt ggaacatcgc 600
45 attgcgagga ccgaccttga caaaggtggc aacagtgttc agctgacgga gcacgctgtt 660
46 gcacatataa cctctgttgt ccctttc                                    687
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49 <211> LENGTH: 229
50 <212> TYPE: PRT
51 <213> ORGANISM: Anemonia majano
53 <400> SEQUENCE: 2
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56 His Met Asp Gly Cys Val Asn Gly His Tyr Phe Thr Val Lys Gly Glu
57             20                  25                  30
58 Gly Asn Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val
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60 Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
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62 Thr Val Phe Lys Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
63 65                    70                    75                    80
64 Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
65                    85                    90                    95
66 Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu
67             100                    105                    110
68 Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly
69         115                    120                    125
70 Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Met Thr Thr Gly
71     130                    135                    140
72 Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys
73 145                    150                    155                    160
74 Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg
75             165                    170                    175
76 Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro
77             180                    185                    190
78 Pro Asn His Ala Val Glu His Arg Ile Ala Arg Thr Asp Leu Asp Lys
79         195                    200                    205
80 Gly Gly Asn Ser Val Gln Leu Thr Glu His Ala Val Ala His Ile Thr
81     210                    215                    220
82 Ser Val Val Pro Phe
83 225
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93 tgcgtcgatg gacataaatt tgtgatcacg ggagagggca ttggatatcc gttcaaaggg 120
94 aaacaggcta ttaatctgtg tgtggtcgaa ggtggaccat tgccatttgc cgaagacata 180
95 ttgtcagctg cctttatgta cggaaacagg gttttcactg aatatcctca agacatagct 240
96 gactatttca agaactcgtg tcctgctggt tatacatggg acaggtcttt tctctttgag 300
97 gatggagcag tttgcatatg taatgcagat ataacagtga gtgttgaaga aaactgcatg 360
98 tatcatgagt ccaaatttta tggagtgaat tttcctgctg atggacctgt gatgaaaaag 420
99 atgacagata actgggagcc atcctgcgag aagatcatac cagtacctaa gcagggata 480
100 ttgaaagggg atgtctccat gtacctcctt ctgaaggatg gtggcgtttt acggtgccaa 540
101 ttcgacacag tttacaaagc aaagtctgtg ccaagaaaga tgccggactg gcacttcatc 600
102 cagcataagc tcacccgtga agaccgcagc gatgctaaga atcagaaatg gcatctgaca 660
103 gaacatgcta ttgcatccgg atctgcattg ccc                                693
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106 <211> LENGTH: 231
107 <212> TYPE: PRT
108 <213> ORGANISM: Zoanthus sp.
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112 1                 5                    10                    15
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114         20              25                  30
115 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val
116         35              40                  45
117 Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala
118     50              55                  60
119 Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Ala
120 65              70                  75                  80
121 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser
122             85                  90                  95
123 Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr
124         100                 105                 110
125 Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys Phe Tyr Gly
126     115                 120                 125
127 Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Asp Asn
128     130                 135                 140
129 Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys Gln Gly Ile
130 145                 150                 155                 160
131 Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg
132             165                 170                 175
133 Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Arg
134         180                 185                 190
135 Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp
136         195                 200                 205
137 Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu His Ala Ile
138     210                 215                 220
139 Ala Ser Gly Ser Ala Leu Pro
140 225                 230
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144 <211> LENGTH: 865
145 <212> TYPE: DNA
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148 <400> SEQUENCE: 5
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150 catggctcat tcaaagcacg gtctaaaaga agaaatgaca atgaaatacc acatggaagg 120
151 gtgcgtcaac ggacataaat ttgtgatcac gggcgaaggc attggatatc cgttcaaagg 180
152 gaaacagact attaatctgt gtgtgatcga agggggacca ttgccatttt ccgaagacat 240
153 attgtcagct ggctttaagt acggagacag gattttcact gaatatcctc aagacatagt 300
154 agactatttc aagaactcgt gtcctgctgg atatacatgg ggcaggtctt ttctctttga 360
155 ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat 420
156 ttatcataag agcatattta atggaatgaa ttttcctgct gatggacctg tgatgaaaaa 480
157 gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat 540
158 actgaaaggg gatgtctcca tgtacctcct tctgaaggat ggtgggcgtt accggtgcca 600
159 gttcgacaca gtttacaaag caaagtctgt gccaagtaag atgccggagt ggcacttcat 660
160 ccagcataag ctcctccgtg aagaccgcag cgatgctaag aatcagaagt ggcagctgac 720
161 agagcatgct attgcattcc cttctgcctt ggcctgataa gaatgtagtt ccaacatttt 780
162 aatgcatgtg cttgtcaatt attctgataa aaatgtagtt gagttgaaaa cagacaagta 840
163 caaataaagc acatgtaaat cgtct                                      865
165 <210> SEQ ID NO: 6
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166 <211> LENGTH: 230
167 <212> TYPE: PRT
168 <213> ORGANISM: Zoanthus sp.
170 <400> SEQUENCE: 6
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172 1               5                   10                  15
173 His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu
174             20                  25                  30
175 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val
176         35                  40                  45
177 Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly
178     50                  55                  60
179 Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val
180 65                  70                  75                  80
181 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Ser Phe
182                 85                  90                  95
183 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val
184             100                 105                 110
185 Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Met
186         115                 120                 125
187 Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp
188     130                 135                 140
189 Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu
190 145                 150                 155                 160
191 Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr
192                 165                 170                 175
193 Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys
194             180                 185                 190
195 Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg
196         195                 200                 205
197 Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala
198     210                 215                 220
199 Phe Pro Ser Ala Leu Ala
200 225                 230
203 <210> SEQ ID NO: 7
204 <211> LENGTH: 678
205 <212> TYPE: DNA
206 <213> ORGANISM: Discosoma sp
208 <400> SEQUENCE: 7
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211 cacaacaccg tgaagctgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180
212 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcaccccgc cgacatcccc 240
213 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgtgat gaacttcgag 300
214 gacggcggcg tggtgaccgt gacccaggac tcctccctgc aggacggctg cttcatctac 360
215 aaggtgaagt tcatcggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420
216 atgggctggg aggcctccac cgagcgcctg taccccgcg acggcgtgct gaagggcgag 480
217 atccacaagg ccctgaagct gaaggacggc ggccactacc tggtggagtt caagtccatc 540
218 tacatggcca agaagcccgt gcagctgccc ggctactact acgtggactc caagctggac 600
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219 atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660
220 caccacctgt tcctgtaa                                               678
222 <210> SEQ ID NO: 8
223 <211> LENGTH: 225
224 <212> TYPE: PRT
225 <213> ORGANISM: Discosoma sp.
227 <400> SEQUENCE: 8
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229  1               5                  10                  15
230 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
231              20                  25                  30
232 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
233              35                  40                  45
234 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
235      50                  55                  60
236 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
237 65                  70                  75                  80
238 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
239                  85                  90                  95
240 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
241              100                 105                 110
242 Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
243              115                 120                 125
244 Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
245      130                 135                 140
246 Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
247 145                 150                 155                 160
248 Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
249              165                 ·170                 175
250 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
251              180                 185                 190
252 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
253              195                 200                 205
254 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
255      210                 215                 220
256 Leu
257 225
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 696
262 <212> TYPE: DNA
263 <213> ORGANISM: Anemonia sulcata
265 <400> SEQUENCE: 9
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267 ggccactact tcaagtgtac aggaaaagga gagggcaacc catttgaggg tacgcaggaa 120
268 atgaagatag aggtcatcga aggaggtcca ttgccatttg ccttccacat tttgtcaacg 180
269 agttgtatgt acggtagtaa ggccttcatc aagtatgtgt caggaattcc tgactacttc 240
270 aagcagtctt tccctgaagg ttttacttgg gaaagaacca caacctacga ggatggaggc 300
271 tttcttacag ctcatcagga cacaagccta gatggagatt gcctcgttta caaggtcaag 360
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VERIFICATION SUMMARY   DATE: 06/28/2002
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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date